



SEQUENCE LISTING

<110> HYBRIGENICS

Pierre, Legrain

<120> Protein-protein interactions in adipocyte cells

<130> B4767A

<140> US 10/038,010

<141> 2002-01-02

<150> US 60/259,377

<151> 2001-01-02

<160> 67

<170> PatentIn version 3.1

<210> 1

<211> 492

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) . . (492)

<223> Human Skp1 : Part of SCF (Skp1/Cullin/F-box) complexes which act as E3 Ubiquitin ligases.

```
<400> 1
atgccttcaa ttaagttgca gagttctgat ggagagatat ttgaagttga tgtggaaatt
```

60

gccaaacaat ctgtaactat taagaccatg ttggaagatt tgggaatgga tgatgaagga 120
 gatgatgacc cagttcctct accaaatgtg aatgcagcaa tattaataaaa ggatcattcag 180
 tgggtgcaccc accacaagga tgaccctcct cctcctgaag atgatgagaa caaagaaaag 240
 cggacagatg atatccctgt ttgggaccaa gaattcctga aagttgacca aggaacactt 300
 tttgaactca ttctggctgc aaactactta gacatcaaag gtttgcttga tgttacatgc 360
 aagactgttg ccaatatgat caaggggaaa actcctgagg agattcgcaa gaccttcaat 420
 atcaaaaatg actttactga agaggaggaa gccaggtac gcaaagagaa ccagtgggtg 480
 gaagagaagt ga 492

<210> 2
 <211> 163
 <212> PRT
 <213> Homo sapiens

<220>
 <221> Skp1
 <222> (1) .. (163)
 <223>

<400> 2
 Met Pro Ser Ile Lys Leu Gln Ser Ser Asp Gly Glu Ile Phe Glu Val
 1 5 10 15
 Asp Val Glu Ile Ala Lys Gln Ser Val Thr Ile Lys Thr Met Leu Glu
 20 25 30
 Asp Leu Gly Met Asp Asp Glu Gly Asp Asp Asp Pro Val Pro Leu Pro
 35 40 45
 Asn Val Asn Ala Ala Ile Leu Lys Lys Val Ile Gln Trp Cys Thr His
 50 55 60
 His Lys Asp Asp Pro Pro Pro Pro Glu Asp Asp Glu Asn Lys Glu Lys
 65 70 75 80
 Arg Thr Asp Asp Ile Pro Val Trp Asp Gln Glu Phe Leu Lys Val Asp

	85	90	95
Gln Gly Thr	Leu Phe Glu Leu Ile Leu Ala Ala Asn Tyr Leu Asp Ile		
	100	105	110
Lys Gly Leu Leu Asp Val Thr Cys Lys Thr Val Ala Asn Met Ile Lys			
	115	120	125
Gly Lys Thr Pro Glu Glu Ile Arg Lys Thr Phe Asn Ile Lys Asn Asp			
	130	135	140
Phe Thr Glu Glu Glu Glu Ala Gln Val Arg Lys Glu Asn Gln Trp Cys			
145	150	155	160

Glu Glu Lys

<210> 3

<211> 1917

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (1917)

<223> Human Splicing Factor 1

<400> 3	
atggcgaccg gagcgaacgc cagccggttg gacttcccaa gtaagaagcg gaagaggagc	60
cgctggaacc aagacacaat ggaacagaag acagtgattc caggaatgcc tacagttatt	120
ccccctggac ttactcgaga acaagaaaga gcttatatag tgcaactgca gatagaagac	180
ctgactcgta aactgcgcac aggagacctg ggcattcccc ctaaccctga ggacagggtcc	240
ccttcccctg agcccatcta caatagcgag gggaagcggc ttaacacccg agagttccgc	300
accgcacaaa agctggaaga ggagcggcac aacctcatca cagagatggg tgcactcaat	360
ccggatttca agccacctgc agattacaaa cctccagcaa cacgtgtgag tgataaagtc	420
atgattccac aagatgagta cccagaaatc aactttgtgg ggctgctcat cgggcccaga	480
gggaacaccc tgaagaacat agagaaggag tgcaatgcca agattatgat ccgggggaaa	540

```

gggtctgtga aagaagggaa ggttgggagc aaagatggcc agatgttgcc aggagaagat   600
gagccacttc atgccctggg tactgccaat acaatggaga acgtcaaaaa ggcagtggaa   660
cagataagaa acatcctgaa gcagggtatc gagactccag aggaccagaa tgatctacgg   720
aagatgcagc ttcgggagtt ggctcgctta aatgggaccc ttcgggaaga cgataacagg   780
atcttaagac cctggcagag ctgagagacc cgcagcatta ccaacaccac agtgtgtacc   840
aagtgtggag gggctggcca cattgcttca gactgtaaat tccaaaggcc tggatgatcct   900
cagtcagctc aggataaagc acggatggat aaagaatatt tgtccctcat ggctgaactg   960
ggtgaagcac ctgtcccagc atctgtgggc tccacctctg ggctgccac cacaccctg  1020
gccagcgcac ctgtcctgct tgtcccgcgc aacaaccac ctccaccgct tctcatgtct  1080
accaccagaa gccgcccacc ctggatgaat tctggccctt cagagagtcg gccctaccac  1140
ggcatgcatg gaggtgggtc tgggtgggccc ggaggtggcc cccacagctt cccacacca  1200
ttaccagacc tgacaggtgg gcatgggtga catcccatgc agcacaaccc caatggaccc  1260
ccaccctctt ggatgcagcc accaccacca ccgatgaacc agggccccca cctcctggg  1320
caccatggcc ctctccaat ggatcagtac ctgggaagta cgctgtggg ctctggggtc  1380
tatcgctgct atcaaggaaa aggtatgatg ccgccaccac ctatgggcat gatgccgccc  1440
ccgcccgcgc ctcccagtg gtagccccc cccctcctct ctgggtcctt tcccccatgg  1500
caacaacagc agcagcagcc tccgccaccc cctccgccc gtagcagtat ggcttccagt  1560
accccttgc catggcagca aaatacagc actaccacca cgagcgctgg cacagggtcc  1620
atcccgccat ggcaacagca gcaggcggct gccgcagctt ctccaggagc cctcagatg  1680
caaggcaacc ccactatggg gccctgccc cccgggggtcc agccgcctct gccgcctggg  1740
gccctcccc ctccgcccgc tccaccgctt ggttccgccc gcatgatgat cctccccgc  1800
ggcggcgatg gcccgagcca tgagagtga gactttccgc gccattggg gacccttcca  1860
ggcagacagc ctgagcaacg cccctgggtg acaggatggg tcggcaaagc agcctga   1917

```

<210> 4

<211> 638

<212> PRT

<213> Homo sapiens

<220>

<221> Human Splicing Factor 1

<222> (1) .. (638)

<223>

<400> 4

```

Met Ala Thr Gly Ala Asn Ala Thr Pro Leu Asp Phe Pro Ser Lys Lys
1          5          10          15

Arg Lys Arg Ser Arg Trp Asn Gln Asp Thr Met Glu Gln Lys Thr Val
          20          25          30

Ile Pro Gly Met Pro Thr Val Ile Pro Pro Gly Leu Thr Arg Glu Gln
          35          40          45

Glu Arg Ala Tyr Ile Val Gln Leu Gln Ile Glu Asp Leu Thr Arg Lys
          50          55          60

Leu Arg Thr Gly Asp Leu Gly Ile Pro Pro Asn Pro Glu Asp Arg Ser
65          70          75          80

Pro Ser Pro Glu Pro Ile Tyr Asn Ser Glu Gly Lys Arg Leu Asn Thr
          85          90          95

Arg Glu Phe Arg Thr Arg Lys Lys Leu Glu Glu Glu Arg His Asn Leu
          100          105          110

Ile Thr Glu Met Val Ala Leu Asn Pro Asp Phe Lys Pro Pro Ala Asp
          115          120          125

Tyr Lys Pro Pro Ala Thr Arg Val Ser Asp Lys Val Met Ile Pro Gln
          130          135          140

Asp Glu Tyr Pro Glu Ile Asn Phe Val Gly Leu Leu Ile Gly Pro Arg
145          150          155          160

Gly Asn Thr Leu Lys Asn Ile Glu Lys Glu Cys Asn Ala Lys Ile Met
          165          170          175

Ile Arg Gly Lys Gly Ser Val Lys Glu Gly Lys Val Gly Arg Lys Asp
          180          185          190

Gly Gln Met Leu Pro Gly Glu Asp Glu Pro Leu His Ala Leu Val Thr
          195          200          205

```

$$A = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}, B = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}, C = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}, D = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

Ala 210	Asn	Thr	Met	Glu	Asn	Val 215	Lys	Lys	Ala	Val	Glu 220	Gln	Ile	Arg	Asn
Ile 225	Leu	Lys	Gln	Gly	Ile 230	Glu	Thr	Pro	Glu	Asp 235	Gln	Asn	Asp	Leu	Arg 240
Lys	Met	Gln	Leu	Arg 245	Glu	Leu	Ala	Arg	Leu 250	Asn	Gly	Thr	Leu	Arg 255	Glu
Asp	Asp	Asn	Arg 260	Ile	Leu	Arg	Pro	Trp 265	Gln	Ser	Ser	Glu	Thr 270	Arg	Ser
Ile	Thr	Asn 275	Thr	Thr	Val	Cys	Thr 280	Lys	Cys	Gly	Gly	Ala 285	Gly	His	Ile
Ala	Ser 290	Asp	Cys	Lys	Phe	Gln 295	Arg	Pro	Gly	Asp	Pro 300	Gln	Ser	Ala	Gln
Asp 305	Lys	Ala	Arg	Met	Asp 310	Lys	Glu	Tyr	Leu	Ser 315	Leu	Met	Ala	Glu	Leu 320
Gly	Glu	Ala	Pro	Val 325	Pro	Ala	Ser	Val	Gly 330	Ser	Thr	Ser	Gly	Pro 335	Ala
Thr	Thr	Pro	Leu 340	Ala	Ser	Ala	Pro	Arg 345	Pro	Ala	Ala	Pro	Ala 350	Asn	Asn
Pro	Pro	Pro 355	Pro	Ser	Leu	Met	Ser 360	Thr	Thr	Gln	Ser	Arg 365	Pro	Pro	Trp
Met 370	Asn	Ser	Gly	Pro	Ser	Glu 375	Ser	Arg	Pro	Tyr	His 380	Gly	Met	His	Gly
Gly 385	Gly	Pro	Gly	Gly	Pro 390	Gly	Gly	Gly	Pro	His 395	Ser	Phe	Pro	His	Pro 400
Leu	Pro	Ser	Leu	Thr 405	Gly	Gly	His	Gly	Gly 410	His	Pro	Met	Gln	His 415	Asn
Pro	Asn	Gly	Pro 420	Pro	Pro	Pro	Trp	Met 425	Gln	Pro	Pro	Pro	Pro 430	Pro	Met
Asn	Gln	Gly 435	Pro	His	Pro	Pro	Gly 440	His	His	Gly	Pro	Pro 445	Pro	Met	Asp

Gln Tyr Leu Gly Ser Thr Pro Val Gly Ser Gly Val Tyr Arg Leu His
450 455 460

Gln Gly Lys Gly Met Met Pro Pro Pro Pro Met Gly Met Met Pro Pro
465 470 475 480

Pro Pro Pro Pro Pro Ser Gly Gln Pro Pro Pro Pro Pro Ser Gly Pro
485 490 495

Leu Pro Pro Trp Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro
500 505 510

Pro Ser Ser Ser Met Ala Ser Ser Thr Pro Leu Pro Trp Gln Gln Asn
515 520 525

Thr Thr Thr Thr Thr Thr Ser Ala Gly Thr Gly Ser Ile Pro Pro Trp
530 535 540

Gln Gln Gln Gln Ala Ala Ala Ala Ala Ser Pro Gly Ala Pro Gln Met
545 550 555 560

Gln Gly Asn Pro Thr Met Val Pro Leu Pro Pro Gly Val Gln Pro Pro
565 570 575

Leu Pro Pro Gly Ala Pro Pro Pro Pro Pro Pro Pro Pro Gly Ser
580 585 590

Ala Gly Met Met Ile Pro Pro Arg Gly Gly Asp Gly Pro Ser His Glu
595 600 605

Ser Glu Asp Phe Pro Arg Pro Leu Val Thr Leu Pro Gly Arg Gln Pro
610 615 620

Gln Gln Arg Pro Trp Trp Thr Gly Trp Phe Gly Lys Ala Ala
625 630 635

<210> 5

<211> 1173

<212> DNA

<213> mouse p53

<220>

<221> gene

<222> (1) .. (1173)

<223> mouse p53 : Tumour suppressor protein

<400> 5

```

atgactgcca tggaggagtc acagtcggat atcagcctcg agctccctct gagccaggag      60
acatttttcag gcttatggaa actacttcct ccagaagata tcctgccatc acctcactgc      120
atggacgatac tgttgctgcc ccaggatggt gaggagtttt ttgaaggccc aagtgaagcc      180
ctccgagtgt caggagctcc tgcagcacag gaccctgtca ccgagacccc tggggccagcg      240
gcccctgccc cagccactcc atggcccctg tcattcttttg tcctttctca aaaaacttac      300
cagggcaact atggcttcca cctgggcttc ctgcagtctg ggacagccaa gtctgttatg      360
tgcaactgact ctctccctcc caataagcta ttctgccagc tggcgaagac gtgccctgtg      420
cagttgtggg tcagcgccac acctccagct gggagccgtg tccgcgccat ggccatctac      480
aagaagtcac agcacatgac ggaggtcgtg agacgctgcc cccaccatga gcgctgctcc      540
gatggatgatg gcctggctcc tccccagcat cttatccggg tgggaaggaaa tttgtatccc      600
gagtatctgg aagacaggca gacttttcgc cacagcgtgg tggtagctta tgagccaccc      660
gaggccggct ctgagtatac caccatccac tacaagtaca tgtgtaatag ctctgcatg      720
gggggcatga accgccgacc tacccttacc atcatcacac tgggaagactc cagtgggaac      780
cttctgggac gggacagctt tgagggttcgt gtttgtgcct gccctgggag agaccgccgt      840
acagaagaag aaaatttccg caaaaaggaa gtcctttgcc ctgaactgcc cccagggagc      900
gcaaagagag cgctgcccac ctgcacaagc gcctctcccc cgcaaaagaa aaaaccactt      960
gatggagagt atttcaccct caagatccgc gggcgtaaac gcttcgagat gttccgggag     1020
ctgaatgagg ccttagagtt aaaggatgcc catgctacag aggagtctgg agacagcagg     1080
gctcactcca gctacctgaa gaccaagaag ggccagtcta cttcccgcga taaaaaaaca     1140
atggtcaaga aagtggggcc tgactcagac tga                                     1173

```

<210> 6

<211> 390

<212> PRT

<213> mouse p53

$\langle 220 \rangle$

<221> p53

<222> (1) .. (390)

<223>

<400> 6

Met Thr Ala Met Glu Glu Ser Gln Ser Asp Ile Ser Leu Glu Leu Pro
1 5 10 15

Leu Ser Gln Glu Thr Phe Ser Gly Leu Trp Lys Leu Leu Pro Pro Glu
20 25 30

Asp Ile Leu Pro Ser Pro His Cys Met Asp Asp Leu Leu Leu Pro Gln
35 40 45

Asp Val Glu Glu Phe Phe Glu Gly Pro Ser Glu Ala Leu Arg Val Ser
50 55 60

Gly Ala Pro Ala Ala Gln Asp Pro Val Thr Glu Thr Pro Gly Pro Ala
65 70 75 80

Ala Pro⁸⁵ Ala Pro Ala Thr Pro Trp Pro Leu⁹⁰ Ser Ser Phe Val Pro⁹⁵ Ser

Gln Lys Thr Tyr Gln Gly Asn Tyr Gly Phe His Leu Gly Phe Leu Gln
100 105 110

Ser Gly Thr Ala Lys Ser Val Met Cys Thr Tyr Ser Pro Pro Leu Asn
115 120 125

Lys Leu Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val
130 135 140

Ser Ala Thr Pro Pro Ala Gly Ser Arg Val Arg Ala Met Ala Ile Tyr
145 150 155 160

Lys Lys Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His
165 170 175

Glu Arg Cys Ser Asp Gly Asp Gly Leu Ala Pro Pro Gln His Leu Ile
180 185 190

Arg Val Glu Gly Asn Leu Tyr Pro Glu Tyr Leu Glu Asp Arg Gln Thr

195					200					205				
Phe	Arg	His	Ser	Val	Val	Pro	Tyr	Glu	Pro	Pro	Glu	Ala	Gly	Ser
210					215					220				
Glu	Tyr	Thr	Thr	Ile	His	Tyr	Lys	Tyr	Met	Cys	Asn	Ser	Ser	Cys
225					230					235				240
Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Thr	Ile	Ile	Thr	Leu	Glu
				245					250					255
Ser	Ser	Gly	Asn	Leu	Leu	Gly	Arg	Asp	Ser	Phe	Glu	Val	Arg	Val
			260					265					270	Cys
Ala	Cys	Pro	Gly	Arg	Asp	Arg	Arg	Thr	Glu	Glu	Glu	Asn	Phe	Arg
		275					280					285		Lys
Lys	Glu	Val	Leu	Cys	Pro	Glu	Leu	Pro	Pro	Gly	Ser	Ala	Lys	Arg
	290					295					300			Ala
Leu	Pro	Thr	Cys	Thr	Ser	Ala	Ser	Pro	Pro	Gln	Lys	Lys	Lys	Pro
305					310					315				320
Asp	Gly	Glu	Tyr	Phe	Thr	Leu	Lys	Ile	Arg	Gly	Arg	Lys	Arg	Phe
				325					330					335
Met	Phe	Arg	Glu	Leu	Asn	Glu	Ala	Leu	Glu	Leu	Lys	Asp	Ala	His
			340					345					350	Ala
Thr	Glu	Glu	Ser	Gly	Asp	Ser	Arg	Ala	His	Ser	Ser	Tyr	Leu	Lys
		355					360					365		Thr
Lys	Lys	Gly	Gln	Ser	Thr	Ser	Arg	His	Lys	Lys	Thr	Met	Val	Lys
	370					375					380			
Val	Gly	Pro	Asp	Ser	Asp									
385					390									

<210> 7

<211> 1710

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(1710)

<223> Human beta-TrCP1 : F-box containing protein with 7 WD40 repeats;
Part of SCF (Skp1/Cullin/F-box) complex E3 ubiquitin ligase; Impl
icated in the degradation of b-catenin and IkBa

```

<400> 7
atggacccgg ccgaggcggg gctgcaagag aaggcactca agtttatgaa ttcctcagag    60
agagaagact gtaataatgg cgaaccccct aggaagataa taccagagaa gaattcactt    120
agacagacat acaacagctg tgccagactc tgcttaaacc aagaaacagt atgttttagca    180
agcactgcta tgaagactga gaattgtgtg gccaaaacaa aacttgccaa tggcacttcc    240
agtatgattg tgcccaagca acggaaactc tcagcaagct atgaaaagga aaaggaactg    300
tgtgtcaa atctttgagca gtgggtcagag tcagatcaag tggaatttgt ggaacatctt    360
atatcccaaa tgtgtcatta ccaacatggg cacataaact cgtatcttaa acctatgttg    420
cagagagatt tcataactgc tctgccagct cggggattgg atcatatcgc tgagaacatt    480
ctgtcatacc tggatgccaa atcactatgt gctgctgaac ttgtgtgcaa ggaatggtac    540
cgagtgcact ctgatggcat gctgtggaag aagcttatcg agagaatggt caggacagat    600
tctctgtgga gaggcctggc agaacgaaga ggatggggac agtatattatt caaaaacaaa    660
cctcctgacg ggaatgctcc tcccaactct ttttatagag cactttatcc taaaattata    720
caagacattg agacaataga atctaattgg agatgtggaa gacatagttt acagagaatt    780
cactgccgaa gtgaaacaag caaaggagtt tactgtttac agtatgatga tcagaaaata    840
gtaagcggcc ttcgagacaa cacaatcaag atctgggata aaaacacatt ggaatgcaag    900
cgaattctca caggccatac aggttcagtc ctctgtctcc agtatgatga gagagtgatc    960
ataacaggat catcggattc cacggtcaga gtgtgggatg taaatacagg tgaaatgcta   1020
aacacgttga ttcaccattg tgaagcagtt ctgcacttgc gtttcaataa tggcatgatg   1080
gtgacctgct ccaaagatcg ttccattgct gtatgggata tggcctcccc aactgacatt   1140
accctccgga ggggtgctgg cggacaccga gctgctgtca atgttgtaga ctttgatgac   1200
aagtacattg tttctgcac tggggataga actataaagg tatggaacac aagtacttgt   1260
gaatttgtaa ggaccttaaa tggacacaaa cgaggcattg cctgtttgca gtacagggac   1320
aggctggtag tgagtggctc atctgacaac actatcagat tatgggacat agaatgtggt   1380
gcatgtttac gagtggttaga aggccatgag gaattggtgc gttgtattcg atttgataac   1440

```

aagaggatag tcagtggggc ctatgatgga aaaattaaag tgtgggatct tgtggctgct 1500
 ttggaccccc gtgctcctgc agggacactc tgtctacgga cccttgtgga gcattccgga 1560
 agagtttttc gactacagtt tgatgaattc cagattgtca gtagttcaca tgatgacaca 1620
 atcctcatct gggacttcct aaatgatcca gctgccaag ctgaaccccc ccgttcccct 1680
 tctcgaacat acacctacat ctccagataa 1710

<210> 8

<211> 569

<212> PRT

<213> Homo sapiens

<220>

<221> beta-TrCP1

<222> (1) .. (569)

<223>

<400> 8

Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met
 1 5 10 15

Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
 20 25 30

Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
 35 40 45

Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
 50 55 60

Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
 65 70 75 80

Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
 85 90 95

Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
 100 105 110

Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
115 120 125

His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
130 135 140

Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
145 150 155 160

Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
165 170 175

Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
180 185 190

Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
195 200 205

Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly
210 215 220

Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
225 230 235 240

Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
245 250 255

Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
260 265 270

Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
275 280 285

Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr
290 295 300

Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile
305 310 315 320

Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr
325 330 335

Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His
340 345 350

Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser

355		360		365											
Ile	Ala	Val	Trp	Asp	Met	Ala	Ser	Pro	Thr	Asp	Ile	Thr	Leu	Arg	Arg
370						375					380				
Val	Leu	Val	Gly	His	Arg	Ala	Ala	Val	Asn	Val	Val	Asp	Phe	Asp	Asp
385					390					395					400
Lys	Tyr	Ile	Val	Ser	Ala	Ser	Gly	Asp	Arg	Thr	Ile	Lys	Val	Trp	Asn
				405					410					415	
Thr	Ser	Thr	Cys	Glu	Phe	Val	Arg	Thr	Leu	Asn	Gly	His	Lys	Arg	Gly
			420					425					430		
Ile	Ala	Cys	Leu	Gln	Tyr	Arg	Asp	Arg	Leu	Val	Val	Ser	Gly	Ser	Ser
		435					440					445			
Asp	Asn	Thr	Ile	Arg	Leu	Trp	Asp	Ile	Glu	Cys	Gly	Ala	Cys	Leu	Arg
450						455					460				
Val	Leu	Glu	Gly	His	Glu	Glu	Leu	Val	Arg	Cys	Ile	Arg	Phe	Asp	Asn
465					470					475					480
Lys	Arg	Ile	Val	Ser	Gly	Ala	Tyr	Asp	Gly	Lys	Ile	Lys	Val	Trp	Asp
				485					490					495	
Leu	Val	Ala	Ala	Leu	Asp	Pro	Arg	Ala	Pro	Ala	Gly	Thr	Leu	Cys	Leu
			500					505					510		
Arg	Thr	Leu	Val	Glu	His	Ser	Gly	Arg	Val	Phe	Arg	Leu	Gln	Phe	Asp
		515					520					525			
Glu	Phe	Gln	Ile	Val	Ser	Ser	Ser	His	Asp	Asp	Thr	Ile	Leu	Ile	Trp
		530				535					540				
Asp	Phe	Leu	Asn	Asp	Pro	Ala	Ala	Gln	Ala	Glu	Pro	Pro	Arg	Ser	Pro
545					550					555					560
Ser	Arg	Thr	Tyr	Thr	Tyr	Ile	Ser	Arg							
				565											

<210> 9

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (579)

<223> human Rac1 : Member of Ras subfamily of RAS small GTPases

<400> 9
atgcaggcca tcaagtgtgt ggtggtggga gacggagctg taggtaaaac ttgcctactg 60
atcagttaca caaccaatgc atttcctgga gaatatatcc ctactgtctt tgacaattat 120
tctgccaatg ttatggtaga tggaaaaccg gtgaatctgg gcttatggga tacagctgga 180
caagaagatt atgacagatt acgcccccta tcctatccgc aaacagatgt gttcttaatt 240
tgcttttccc ttgtgagtcc tgcattcattt gaaaatgtcc gtgcaaagtg gtatcctgag 300
gtgcgggcacc actgtcccaa cactcccatc atcctagtgg gaactaaact tgatcttagg 360
gatgataaag acacgatcga gaaactgaag gagaagaagc tgactcccat cacctatccg 420
caggggtctag ccatggctaa ggagattggg gctgtaaaat acctggagtg ctcggcgctc 480
acacagcgag gcctcaagac agtgtttgac gaagcgatcc gagcagtcct ctgccccgct 540
cccgtgaaga agaggaagag aaaatgcctg ctgttgtaa 579

<210> 10

<211> 192

<212> PRT

<213> Homo sapiens

<220>

<221> Rac1

<222> (1) .. (192)

<223>

<400> 10

Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys
1 5 10 15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly Glu Tyr
20 25 30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val Asp Gly
35 40 45

Lys Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr
50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile
65 70 75 80

Cys Phe Ser Leu Val Ser Pro Ala Ser Phe Glu Asn Val Arg Ala Lys
85 90 95

Trp Tyr Pro Glu Val Arg His His Cys Pro Asn Thr Pro Ile Ile Leu
100 105 110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys
115 120 125

Leu Lys Glu Lys Lys Leu Thr Pro Ile Thr Tyr Pro Gln Gly Leu Ala
130 135 140

Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser Ala Leu
145 150 155 160

Thr Gln Arg Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val
165 170 175

Leu Cys Pro Pro Pro Val Lys Lys Arg Lys Arg Lys Cys Leu Leu Leu
180 185 190

<210> 11
<211> 915
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (1) .. (915)

<223> Human uracil DNA glycosylase : Uracil DNA glycosylase implicated in DNA repair

<400> 11
atgggcgtct tctgccttgg gccgtggggg ttgggcccga agctgcggac gcctgggaag 60
gggccgctgc agctcttgag ccgcctctgc ggggaccact tgcaggccat cccagccaag 120
aaggccccgg ctgggcagga ggagcctggg acgccgccct cctcgccgct gagtgccgag 180
cagttggacc ggatccagag gaacaaggcc gcggccctgc tcagactcgc ggcccgcaac 240
gtgcccgtgg gctttggaga gagctggaag aagcacctca gcggggagtt cgggaaaccg 300
tattttatca agctaattggg atttggtgca gaagaaagaa agcattacac tgtttatcca 360
ccccacacc aagtcttcac ctggaccag atgtgtgaca taaaagatgt gaagggtgtc 420
atcctgggac aggatccata tcatggacct aatcaagctc acgggctctg ctttagtggt 480
caaaggcctg ttccgcctcc gccagtttg gagaacattt ataaagagtt gtctacagac 540
atagaggatt ttgttcatcc tggccatgga gatttatctg ggtgggcca gcaagggtgt 600
ctccttctca acgctgtcct cacggttcgt gcccatcaag ccaactctca taaggagcga 660
ggctgggagc agttcactga tgcagttgtg tcctggctaa atcagaactc gaatggcctt 720
gttttcttgc tctggggctc ttatgctcag aagaagggca gtgccattga taggaagcgg 780
caccatgtac tacagacggc tcatccctcc cttttgtcag tgtatagagg gttcttttga 840
tgtagacact tttcaaagac caatgagctg ctgcagaagt ctggcaagaa gccattgac 900
tggaaggagc tgtga 915

<210> 12

<211> 304

<212> PRT

<213> Homo sapiens

<220>

<221> DNA glycosylase

<222> (1) .. (304)

<223>

<400> 12

Met Gly Val Phe Cys Leu Gly Pro Trp Gly Leu Gly Arg Lys Leu Arg
1 5 10 15

Thr Pro Gly Lys Gly Pro Leu Gln Leu Leu Ser Arg Leu Cys Gly Asp
20 25 30

His Leu Gln Ala Ile Pro Ala Lys Lys Ala Pro Ala Gly Gln Glu Glu
35 40 45

Pro Gly Thr Pro Pro Ser Ser Pro Leu Ser Ala Glu Gln Leu Asp Arg
50 55 60

Ile Gln Arg Asn Lys Ala Ala Ala Leu Leu Arg Leu Ala Ala Arg Asn
65 70 75 80

Val Pro Val Gly Phe Gly Glu Ser Trp Lys Lys His Leu Ser Gly Glu
85 90 95

Phe Gly Lys Pro Tyr Phe Ile Lys Leu Met Gly Phe Val Ala Glu Glu
100 105 110

Arg Lys His Tyr Thr Val Tyr Pro Pro His Gln Val Phe Thr Trp
115 120 125

Thr Gln Met Cys Asp Ile Lys Asp Val Lys Val Val Ile Leu Gly Gln
130 135 140

Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val
145 150 155 160

Gln Arg Pro Val Pro Pro Pro Pro Ser Leu Glu Asn Ile Tyr Lys Glu
165 170 175

Leu Ser Thr Asp Ile Glu Asp Phe Val His Pro Gly His Gly Asp Leu
180 185 190

Ser Gly Trp Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val Leu Thr
195 200 205

Val Arg Ala His Gln Ala Asn Ser His Lys Glu Arg Gly Trp Glu Gln
210 215 220

Phe Thr Asp Ala Val Val Ser Trp Leu Asn Gln Asn Ser Asn Gly Leu
225 230 235 240

Val Phe Leu Leu Trp Gly Ser Tyr Ala Gln Lys Lys Gly Ser Ala Ile

245 250 255

Asp Arg Lys Arg His His Val Leu Gln Thr Ala His Pro Ser Pro Leu
260 265 270

Ser Val Tyr Arg Gly Phe Phe Gly Cys Arg His Phe Ser Lys Thr Asn
275 280 285

Glu Leu Leu Gln Lys Ser Gly Lys Lys Pro Ile Asp Trp Lys Glu Leu
290 295 300

<210> 13

<211> 158

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (158)

<223> Human b2 adrenergic receptor : Oncogene

<400> 13

tctttcagga ggccaaaagg cagctccaga agattgacaa atctgagggc cgcttccatg 60

tccagaacct tagccaggtg gagcaggatg ggcggacggg gcatggactc cgcagatctt 120

ccaagttctg cttgaaggag caciaagccc tcaagtga 158

<210> 14

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> b2 adrenergic receptor

<222> (1) .. (52)

<223>

<400> 14

Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu
1 5 10 15
Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg
20 25 30
Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His
35 40 45
Lys Ala Leu Lys
50

<210> 15

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(261)

<223> Human b2 adrenergic receptor : Oncogene

<400> 15
cggagcccag atttcaggat tgccttccag gagcttctgt gcctgcgcag gtcttctttg 60
aaggcctatg gcaatggcta ctccagcaac ggcaacacag gggagcagag tggatatcac 120
gtggaacagg agaaagaaaa taaactgctg tgtgaagacc tcccaggcac ggaagacttt 180
gtggggccatc aagggtactgt gcctagcgat aacattgatt cacaagggag gaattgtagt 240
acaaatgact cactgctata a 261

<210> 16

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> b2 adrenergic receptor

<222> (1) .. (86)

<223>

<400> 16

Arg Ser Pro Asp Phe Arg Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg
1 5 10 15

Arg Ser Ser Leu Lys Ala Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn
20 25 30

Thr Gly Glu Gln Ser Gly Tyr His Val Glu Gln Glu Lys Glu Asn Lys
35 40 45

Leu Leu Cys Glu Asp Leu Pro Gly Thr Glu Asp Phe Val Gly His Gln
50 55 60

Gly Thr Val Pro Ser Asp Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser
65 70 75 80

Thr Asn Asp Ser Leu Leu
85

<210> 17

<211> 423

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (423)

<223> Human b2 adrenergic receptor : Oncogene

<400> 17

gtcttttcagg aggccaaaag gcagctccag aagattgaca aatctgaggg ccgcttccat 60

```

gtccagaacc ttagccaggt ggagcaggat gggcggacgg ggcattggact ccgcagatct    120
tccaagttct gcttgaagga gcacaaagcc ctcaagggat cccggagccc agatttcagg    180
attgccttcc aggagcttct gtgcctgcgc aggtcttctt tgaaggccta tggcaatggc    240
tactccagca acggcaacac aggggagcag agtggatatc acgtggaaca ggagaaagaa    300
aataaactgc tgtgtgaaga cctcccaggc acggaagact ttgtggggcca tcaaggtact    360
gtgcctagcg ataacattga ttcacaaggg aggaattgta gtacaaatga ctactgcta    420
taa                                                                    423

```

<210> 18

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> b2 adrenergic receptor

<222> (1)..(140)

<223>

<400> 18

```

Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu
1          5          10          15

```

```

Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg
          20          25          30

```

```

Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His
          35          40          45

```

```

Lys Ala Leu Lys Gly Ser Arg Ser Pro Asp Phe Arg Ile Ala Phe Gln
          50          55          60

```

```

Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn Gly
65          70          75          80

```

```

Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val Glu
          85          90          95

```

Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr Glu
100 105 110

Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp Ser
115 120 125

Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
130 135 140

<210> 19

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (579)

<223> Human b2 adrenergic receptor : Oncogene

<400> 19
gtcttttcagg aggccaaaag gcagctccag aagattgaca aatctgaggg ccgcttccat 60
gtccagaacc ttagccaggt ggagcaggat gggcggacgg ggcattggact ccgcagatct 120
tccaagttct gcttgaagga gcacaaagcc ctcaagacgt taggcatcat catggggcact 180
ttcaccctct gctggctgcc cttcttcacg gttaacattg tgcattgtgat ccaggataac 240
ctcatccgta aggaagttta catcctccta aattggatag gctatgtcaa ttctgggttc 300
aatcccctta tctactgccg gagcccagat ttcaggattg ccttccagga gcttctgtgc 360
ctgctgcagg cttcttttgaa ggcctatggc aatggctact ccagcaacgg caacacaggg 420
gagcagagtg gatatcacgt ggaacaggag aaagaaaata aactgctgtg tgaagacctc 480
ccaggcacgg aagactttgt gggccatcaa ggtactgtgc ctagcgataa cattgattca 540
caagggagga attgtagtac aaatgactca ctgctataa 579

<210> 20

<211> 192

<212> PRT

<213> Homo sapiens

<220>

<221> b2 adrenergic receptor

<222> (1) .. (192)

<223>

<400> 20

Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu
1 5 10 15

Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg
20 25 30

Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His
35 40 45

Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys
50 55 60

Trp Leu Pro Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn
65 70 75 80

Leu Ile Arg Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val
85 90 95

Asn Ser Gly Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg
100 105 110

Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala
115 120 125

Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly
130 135 140

Tyr His Val Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu
145 150 155 160

Pro Gly Thr Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp
165 170 175

Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu

	180	185	190
<210>	21		
<211>	1794		
<212>	DNA		
<213>	Homo sapiens		
<220>			
<221>	gene		
<222>	(1) .. (1794)		
<223>	hSHP2_FL		
<400>	21		
	atgacatcgc ggagatgggtt tcacccaaat atcactgggtg tggaggcaga aaacctactg		60
	ttgacaagag gagttaatgg cagtttttttg gcaaggccta gtaaaagtaa ccctggagac		120
	ttcacacttt ccgttagaag aaatggagct gtcaccacaca tcaagattca gaacactgggt		180
	gattactatg acctgtatgg aggggagaaa tttgccactt tggctgagtt ggtccagtat		240
	tacatggaac atcacgggca attaaaagag aagaatggag atgtcattga gcttaaatat		300
	cctctgaact gtgcagatcc tacctctgaa aggtgggtttc atggacatct ctctgggaaa		360
	gaagcagaga aattattaac tgaaaaagga aaacatggta gttttcttgt acgagagagc		420
	cagagccacc ctggagatth tgttctttct gtgcgcactg gtgatgacaa aggggagagc		480
	aatgacggca agtctaaagt gacccatggt atgattcgct gtcaggaact gaaatacgac		540
	gttgggtggag gagaacgggt tgattctttg acagatcttg tggaacatta taagaagaat		600
	cctatgggtgg aaacattggg tacagtacta caactcaagc agccccttaa cacgactcgt		660
	ataaatgctg ctgaaataga aagcagagtt cgagaactaa gcaaattagc tgagaccaca		720
	gataaagtca aacaaggctt ttgggaagaa tttgagacac tacaacaaca ggagtgcaaa		780
	cttctctaca gccgaaaaga ggggtcaaagg caagaaaaca aaaacaaaaa tagatataaa		840
	aacatcctgc cctttgatca taccagggtt gtcctacacg atgggtgatcc caatgagcct		900
	gtttcagatt acatcaatgc aaatatcatc atgcctgaat ttgaaaccaa gtgcaacaat		960
	tcaaagccca aaaagagtta cattgccaca caaggctgcc tgcaaaacac ggtgaatgac		1020
	ttttggcgga tgggtgttcca agaaaactcc cgagtgattg tcatgacaac gaaagaagtg		1080
	gagagaggaa agagtaaagt tgtcaaatac tggcctgatg agtatgctct aaaagaatat		1140

Ile Asn Ala Asn Ile Ile Met Pro Glu Phe Glu Thr Lys Cys Asn Asn
305 310 315 320

Ser Lys Pro Lys Lys Ser Tyr Ile Ala Thr Gln Gly Cys Leu Gln Asn
325 330 335

Thr Val Asn Asp Phe Trp Arg Met Val Phe Gln Glu Asn Ser Arg Val
340 345 350

Ile Val Met Thr Thr Lys Glu Val Glu Arg Gly Lys Ser Lys Cys Val
355 360 365

Lys Tyr Trp Pro Asp Glu Tyr Ala Leu Lys Glu Tyr Gly Val Met Arg
370 375 380

Val Arg Asn Val Lys Glu Ser Ala Ala His Asp Tyr Thr Leu Arg Glu
385 390 395 400

Leu Lys Leu Ser Lys Val Gly Gln Ala Leu Leu Gln Gly Asn Thr Glu
405 410 415

Arg Thr Val Trp Gln Tyr His Phe Arg Thr Trp Pro Asp His Gly Val
420 425 430

Pro Ser Asp Pro Gly Gly Val Leu Asp Phe Leu Glu Glu Val His His
435 440 445

Lys Gln Glu Ser Ile Met Asp Ala Gly Pro Val Val Val His Cys Ser
450 455 460

Ala Gly Ile Gly Arg Thr Gly Thr Phe Ile Val Ile Asp Ile Leu Ile
465 470 475 480

Asp Ile Ile Arg Glu Lys Gly Val Asp Cys Asp Ile Asp Val Pro Lys
485 490 495

Thr Ile Gln Met Val Arg Ser Gln Arg Ser Gly Met Val Gln Thr Glu
500 505 510

Ala Gln Tyr Arg Phe Ile Tyr Met Ala Val Gln His Tyr Ile Glu Thr
515 520 525

Leu Gln Arg Arg Ile Glu Glu Glu Gln Lys Ser Lys Arg Lys Gly His
530 535 540

Glu Tyr Thr Asn Ile Lys Tyr Ser Leu Ala Asp Gln Thr Ser Gly Asp

545 550 555 560

Gln Ser Pro Leu Pro Pro Cys Thr Pro Thr Pro Pro Cys Ala Glu Met
565 570 575

Arg Glu Asp Ser Ala Arg Val Tyr Glu Asn Val Gly Leu Met Gln Gln
580 585 590

Gln Lys Ser Phe Arg
595

<210> 23

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(396)

<223> Human OBRGRP

<400> 23

atggcgggcg ttaaagctct cgtggcatta tccttcagtg gggctattgg actgactttt 60
cttatgctgg gatgtgcctt agaggattat ggcgtttact ggccttatt cgtcctgatt 120
ttccacgcca tctcccccat cccccatttc attgccaaaa gagtcaccta tgactcagat 180
gcaaccagta gtgcctgtcg ggaactggca tatttcttca ctactggaat tgttgtttct 240
gcctttggat ttctgttat tcttgctcgt gtggctgtga tcaaatgggg agcctgcggc 300
cttgtgttgg caggcaatgc agtcattttc cttacaattc aagggttttt cttatatatt 360
ggaagaggag atgatttttag ctgggagcag tggtag 396

<210> 24

<211> 131

<212> PRT

<213> Homo sapiens

<220>

<221> OBRGRP

<222> (1) .. (131)

<223>

<400> 24

Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
1 5 10 15

Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
20 25 30

Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
35 40 45

His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
50 55 60

Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
65 70 75 80

Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
85 90 95

Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
100 105 110

Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
115 120 125

Glu Gln Trp
130

<210> 25

<211> 114

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (114)

<223> Human OBRGRP

<400> 25

attgccaaaa gagtcaccta tgactcagat gcaaccagta gtgcctgtcg ggaactggca 60

tatggatccc ttatatattgg aagaggagat gatttttagct gggagcagtg gtag 114

<210> 26

<211> 37

<212> PRT

<213> Homo sapiens

<220>

<221> OBRGRP

<222> (1) .. (37)

<223>

<400> 26

Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser Ala Cys
1 5 10 15

Arg Glu Leu Ala Tyr Gly Ser Leu Ile Phe Gly Arg Gly Asp Asp Phe
20 25 30

Ser Trp Glu Gln Trp
35

<210> 27

<211> 87

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(87)

<223> Human Melatonin 1a receptor

<400> 27
ggcatcgcca tcaaccgcta ctgctacatc tgccacagtc tcaagtagca caaactgtac 60
agcagcaaga actccctctg ctactag 87

<210> 28

<211> 28

<212> PRT

<213> Homo sapiens

<220>

<221> Melatonin 1a receptor

<222> (1)..(28)

<223>

<400> 28

Gly Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys His Ser Leu Lys Tyr
1 5 10 15

Asp Lys Leu Tyr Ser Ser Lys Asn Ser Leu Cys Tyr
20 25

<210> 29

<211> 90

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(90)

<223> Human Melatonin 1a receptor

[illegible]

```
<400> 29
ctggttctcc aggtcagaca gagggtgaaa cctgaccgca aacccaaact gaaaccacag      60
gacttcagga attttgtcac catgttttag                                         90
```

<210> 30

<211> 29

<212> PRT

<213> Homo sapiens

<220>

<221> Melatonin 1a receptor

<222> (1) .. (29)

<223>

<400> 30

Leu Val Leu Gln Val Arg Gln Arg Val Lys Pro Asp Arg Lys Pro Lys
1 5 10 15

Leu Lys Pro Gln Asp Phe Arg Asn Phe Val Thr Met Phe
20 25

<210> 31

<211> 171

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (171)

<223> Human Melatonin 1a receptor

```
<400> 31
tacgggctac tgaaccaaaa tttcaggaag gaatacagga gaattatagt ctcgctctgt      60
```

acagccaggg tggtctttgt ggacagctct aacgacgtgg ccgatagggt taaatggaaa 120
ccgtctccac tgatgaccaa caataatgta gtaaagggtg actccgttta a 171

<210> 32
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> Melatonin 1a receptor
<222> (1)..(56)
<223>

<400> 32
Tyr Gly Leu Leu Asn Gln Asn Phe Arg Lys Glu Tyr Arg Arg Ile Ile
1 5 10 15
Val Ser Leu Cys Thr Ala Arg Val Phe Phe Val Asp Ser Ser Asn Asp
20 25 30
Val Ala Asp Arg Val Lys Trp Lys Pro Ser Pro Leu Met Thr Asn Asn
35 40 45
Asn Val Val Lys Val Asp Ser Val
50 55

<210> 33
<211> 87
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (1)..(87)
<223> Human melatonin 1b receptor

<400> 33
gccatcgcca ttaaccgcta ctgctacatc tgccacagca tggcctacca ccgaatctac 60
cggcgctggc acacccctct gcactga 87

<210> 34
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> melatonin 1b receptor
<222> (1)..(28)
<223>

<400> 34
Ala Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys His Ser Met Ala Tyr
1 5 10 15
His Arg Ile Tyr Arg Arg Trp His Thr Pro Leu His
20 25

<210> 35
<211> 90
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (1)..(90)
<223> Human melatonin 1b receptor

<400> 35
ctggtgcttc aggcccgcag gaaagccaag ccagagagca ggctgtgcct gaagcccagc 60

gacttgcgga gctttctaac catgttttga

90

<210> 36

<211> 29

<212> PRT

<213> Homo sapiens

<220>

<221> melatonin 1b receptor

<222> (1)..(29)

<223>

<400> 36

Leu	Val	Leu	Gln	Ala	Arg	Arg	Lys	Ala	Lys	Pro	Glu	Ser	Arg	Leu	Cys
1			5					10						15	

Leu	Lys	Pro	Ser	Asp	Leu	Arg	Ser	Phe	Leu	Thr	Met	Phe
			20					25				

<210> 37

<211> 168

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(168)

<223> Human melatonin 1b receptor

<400> 37

tatgggctct tgaacaaaaa cttccgcagg gaatacaaga ggatcctctt ggcccttttg 60

aacccacggc actgcattca agatgcttcc aagggcagcc acgcggaggg gctgcagagc 120

ccagctccac ccatcattgg tgtgcagcac caggcagatg ctctctag 168

<210> 38

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> melatonin 1b receptor

<222> (1)..(55)

<223>

<400> 38

Tyr Gly Leu Leu Asn Gln Asn Phe Arg Arg Glu Tyr Lys Arg Ile Leu
1 5 10 15

Leu Ala Leu Trp Asn Pro Arg His Cys Ile Gln Asp Ala Ser Lys Gly
20 25 30

Ser His Ala Glu Gly Leu Gln Ser Pro Ala Pro Pro Ile Ile Gly Val
35 40 45

Gln His Gln Ala Asp Ala Leu
50 55

<210> 39

<211> 120

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(120)

<223> Human OB-receptor short form

<400> 39

ggaacattat taatatacaca ccaaagaatg aaaaagctat tttgggaaga tgttccgaac 60

cccaagaatt gttcctgggc acaaggactt aattttcaga agagaacgga cattctttga 120

<210> 40

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> OB-receptor short form

<222> (1)..(39)

<223>

<400> 40

Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Glu
1				5					10					15	

Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	Trp	Ala	Gln	Gly	Leu	Asn	Phe
			20					25					30		

Gln	Lys	Arg	Thr	Asp	Ile	Leu
						35

<210> 41

<211> 402

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(402)

<223> hOB-receptor long form

<400> 41

ggaacattat taatatcaca ccaaagaatg aaaaagctat tttgggaaga tggtccgaac 60

[illegible]

cccaagaatt gttcctgggc acaaggactt aattttcaga agccagaaaac gtttgagcat	120
ctttttatca agcatacagc atcagtgaca tgtggtcctc ttcttttgga gcctgaaaca	180
atttcagaag atatcagtgt tgatacatca tggaaaaata aagatgagat gatgccaaca	240
actgtggtct ctctactttc aacaacagat cttgaaaagg gttctgtttg tattagtgac	300
cagttcaaca gtgttaactt ctctgaggct gaggggtactg aggtaaccta tgaggacgaa	360
agccagagac aaccctttgt taaatacgcc acgctgatct ag	402

<210> 42

<211> 133

<212> PRT

<213> Homo sapiens

<220>

<221> hOB-receptor long form

<222> (1) .. (133)

<223>

<400> 42

Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu Phe Trp Glu
1 5 10 15

Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly Leu Asn Phe
20 25 30

Gln Lys Pro Glu Thr Phe Glu His Leu Phe Ile Lys His Thr Ala Ser
35 40 45

Val Thr Cys Gly Pro Leu Leu Leu Glu Pro Glu Thr Ile Ser Glu Asp
50 55 60

Ile Ser Val Asp Thr Ser Trp Lys Asn Lys Asp Glu Met Met Pro Thr
65 70 75 80

Thr Val Val Ser Leu Leu Ser Thr Thr Asp Leu Glu Lys Gly Ser Val
85 90 95

Cys Ile Ser Asp Gln Phe Asn Ser Val Asn Phe Ser Glu Ala Glu Gly
100 105 110

Thr Glu Val Thr Tyr Glu Asp Glu Ser Gln Arg Gln Pro Phe Val Lys
 115 120 125

Tyr Ala Thr Leu Ile
 130

<210> 43

<211> 540

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (540)

<223> hOB-receptor long form

<400> 43
 gccacgctga tcagcaactc taaaccaagt gaaactgggtg aagaacaagg gcttataaat 60
 agttcagtca ccaagtgcct ctctagcaaa aattctccat tgaaggattc tttctctaata 120
 agctcatggg agatagaggc ccaggcattt tttatattat cagatcagca tcccaacata 180
 atttcaccac acctcacatt ctcagaagga ttggatgaac ttttgaaatt ggagggaat 240
 ttccctgaag aaaataatga taaaaagtct atctattatt taggggtcac ctcaatcaaa 300
 aagagagaga gtggtgtgct ttgactgac aagtcaaggg tatcgtgccc attcccagcc 360
 ccctgtttat tcacggacat cagagttctc caggacagtt gctcacactt tgtagaaaat 420
 aatatcaact taggaacttc tagtaagaag acttttgcac cttacatgcc tcaattccaa 480
 acttggttcta ctcagactca taagatcatg gaaaacaaga tgtgtgacct aactgtgtaa 540

<210> 44

<211> 179

<212> PRT

<213> Homo sapiens

<220>

<221> hOB-receptor long form

<222> (1) .. (179)

<223>

<400> 44

Ala	Thr	Leu	Ile	Ser	Asn	Ser	Lys	Pro	Ser	Glu	Thr	Gly	Glu	Glu	Gln	1	5	10	15
Gly	Leu	Ile	Asn	Ser	Ser	Val	Thr	Lys	Cys	Phe	Ser	Ser	Lys	Asn	Ser	20	25	30	
Pro	Leu	Lys	Asp	Ser	Phe	Ser	Asn	Ser	Ser	Trp	Glu	Ile	Glu	Ala	Gln	35	40	45	
Ala	Phe	Phe	Ile	Leu	Ser	Asp	Gln	His	Pro	Asn	Ile	Ile	Ser	Pro	His	50	55	60	
Leu	Thr	Phe	Ser	Glu	Gly	Leu	Asp	Glu	Leu	Leu	Lys	Leu	Glu	Gly	Asn	65	70	75	80
Phe	Pro	Glu	Glu	Asn	Asn	Asp	Lys	Lys	Ser	Ile	Tyr	Tyr	Leu	Gly	Val	85	90	95	
Thr	Ser	Ile	Lys	Lys	Arg	Glu	Ser	Gly	Val	Leu	Leu	Thr	Asp	Lys	Ser	100	105	110	
Arg	Val	Ser	Cys	Pro	Phe	Pro	Ala	Pro	Cys	Leu	Phe	Thr	Asp	Ile	Arg	115	120	125	
Val	Leu	Gln	Asp	Ser	Cys	Ser	His	Phe	Val	Glu	Asn	Asn	Ile	Asn	Leu	130	135	140	
Gly	Thr	Ser	Ser	Lys	Lys	Thr	Phe	Ala	Ser	Tyr	Met	Pro	Gln	Phe	Gln	145	150	155	160
Thr	Cys	Ser	Thr	Gln	Thr	His	Lys	Ile	Met	Glu	Asn	Lys	Met	Cys	Asp	165	170	175	
Leu	Thr	Val																	

<210> 45
 <211> 927
 <212> DNA
 <213> Homo sapiens

<220>
 <221> gene
 <222> (1)..(927)
 <223> hOB-receptor long form

<400> 45
 ggaacattat taatatcaca ccaaagaatg aaaaagctat tttgggaaga tgttccgaac 60
 cccaagaatt gttcctgggc acaaggactt aattttcaga agccagaaac gtttgagcat 120
 ctttttatca agcatacagc atcagtgaca tgtgggtcctc ttcttttgga gcctgaaaca 180
 atttcagaag atatcagtgt tgatacatca tggaaaaata aagatgagat gatgccaca 240
 actgtggtct ctctactttc aacaacagat cttgaaaagg gttctgtttg tattagtac 300
 cagttcaaca gtgttaactt ctctgaggct gaggggtactg aggtaaccta tgaggacgaa 360
 agccagagac aaccctttgt taaatacgcc acgctgatca gcaactctaa accaagtga 420
 actggtgaag aacaagggtt tataaatagt tcagtcacca agtgcttctc tagcaaaaat 480
 tctccattga aggattcttt ctctaatagc tcatgggaga tagaggccca ggcatttttt 540
 atattatcag atcagcatcc caacataatt tcaccacacc tcacattctc agaaggattg 600
 gatgaacttt tgaaattgga gggaaatttc cctgaagaaa ataatagata aaagtctatc 660
 tattatttag gggtcacctc aatcaaaaag agagagagtg gtgtgctttt gactgacaag 720
 tcaagggtat cgtgcccatt cccagcccc tgtttattca cggacatcag agttctccag 780
 gacagttgct cacactttgt agaaaataat atcaacttag gaacttctag taagaagact 840
 tttgcatctt acatgcctca attccaaact tgttctactc agactcataa gatcatggaa 900
 aacaagatgt gtgacctaac tgtgtaa 927

<210> 46
 <211> 308
 <212> PRT

<213> Homo sapiens

<220>

<221> hOB-receptor long form

<222> (1) .. (308)

<223>

<400> 46

Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu Phe Trp Glu
1 5 10 15

Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly Leu Asn Phe
20 25 30

Gln Lys Pro Glu Thr Phe Glu His Leu Phe Ile Lys His Thr Ala Ser
35 40 45

Val Thr Cys Gly Pro Leu Leu Leu Glu Pro Glu Thr Ile Ser Glu Asp
50 55 60

Ile Ser Val Asp Thr Ser Trp Lys Asn Lys Asp Glu Met Met Pro Thr
65 70 75 80

Thr Val Val Ser Leu Leu Ser Thr Thr Asp Leu Glu Lys Gly Ser Val
85 90 95

Cys Ile Ser Asp Gln Phe Asn Ser Val Asn Phe Ser Glu Ala Glu Gly
100 105 110

Thr Glu Val Thr Tyr Glu Asp Glu Ser Gln Arg Gln Pro Phe Val Lys
115 120 125

Tyr Ala Thr Leu Ile Ser Asn Ser Lys Pro Ser Glu Thr Gly Glu Glu
130 135 140

Gln Gly Leu Ile Asn Ser Ser Val Thr Lys Cys Phe Ser Ser Lys Asn
145 150 155 160

Ser Pro Leu Lys Asp Ser Phe Ser Asn Ser Ser Trp Glu Ile Glu Ala
165 170 175

Gln Ala Phe Phe Ile Leu Ser Asp Gln His Pro Asn Ile Ile Ser Pro

180	185	190
His Leu Thr Phe Ser Glu Gly	Leu Asp Glu Leu Leu Lys Leu Glu Gly	
195	200	205
Asn Phe Pro Glu Glu Asn Asn Asp Lys Lys Ser	Ile Tyr Tyr Leu Gly	
210	215	220
Val Thr Ser Ile Lys Lys Arg Glu Ser Gly	Val Leu Leu Thr Asp Lys	
225	230	235
Ser Arg Val Ser Cys Pro Phe Pro Ala Pro Cys	Leu Phe Thr Asp Ile	
245	250	255
Arg Val Leu Gln Asp Ser Cys Ser His Phe Val Glu	Asn Asn Ile Asn	
260	265	270
Leu Gly Thr Ser Ser Lys Lys Thr Phe Ala Ser Tyr	Met Pro Gln Phe	
275	280	285
Gln Thr Cys Ser Thr Gln Thr His Lys Ile Met	Glu Asn Lys Met Cys	
290	295	300
Asp Leu Thr Val		
305		

<210> 47

<211> 2070

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(2070)

<223> Human ADBR kinase 1

<400> 47

atggcggacc tggaggcggt gctggccgac gtagagctacc tgatggccat ggagaagagc 60

aaggccacgc cggccgcgcg cgccagcaag aagatactgc tgcccagagcc cagcatccgc 120

agtgtcatgc agaagtacct ggaggaccgg ggcgaggtga cctttgagaa gatcttttcc 180

cagaagctgg ggtacctgct cttccgagac ttctgcctga accacctgga ggaggccagg 240
cccttggtgg aattctatga ggagatcaag aagtacgaga agctggagac ggaggaggag 300
cgtgtggccc gcagccggga gatcttcgac tcatacatca tgaaggagct gctggcctgc 360
tcgcatccct tctcgaagag tgccactgag catgtccaag gccacctggg gaagaagcag 420
gtgcctccgg atctcttcca gccatacatc gaagagattt gtcaaaacct ccgagggggac 480
gtgttccaga aattcattga gagcgataag ttcacacggg tttgccagtg gaagaatgtg 540
gagctcaaca tccacctgac catgaatgac ttcagcgtgc atcgcatcat tgggcgcggg 600
ggctttggcg aggtctatgg gtgccggaag gctgacacag gcaagatgta cgccatgaag 660
tgcttggaaca aaaagcgcac caagatgaag cagggggaga ccctggccct gaacgagcgc 720
atcatgctct cgctcgtcag cactggggac tgcccattca ttgtctgcat gtcatacgcg 780
ttccacacgc cagacaagct cagcttcac cctggacctca tgaacgggtgg ggacctgcac 840
taccacctct ccagcacgg ggtcttctca gaggetgaca tgcgcttcta tgcggccgag 900
atcatcctgg gcctggagca catgcacaac cgcttcgtgg tctaccggga cctgaagcca 960
gccaacatcc ttctggacga gcatggccac gtgcggatct cggacctggg cctggcctgt 1020
gacttctcca agaagaagcc ccatgccagc gtgggcaccc acgggtacat ggctccggag 1080
gtcctgcaga agggcgtggc ctacgacagc agtgccgact gggtctctct ggggtgcatg 1140
ctcttcaagt tgctgcgggg gcacagcccc ttccggcagc acaagaccaa agacaagcat 1200
gagatcgacc gcatgacgct gacgatggcc gtggagctgc ccgactcctt ctcccctgaa 1260
ctacgctccc tgctggaggg gttgctgcag agggatgtca accggagatt gggctgcctg 1320
ggccgagggg ctcaggaggt gaaagagagc ccctttttcc gctccctgga ctggcagatg 1380
gtcttcttgc agaagtaccc tccccgctg atccccccac gaggggaggt gaacgcggcc 1440
gacgccttcg acattggctc cttcgatgag gaggacacaa aaggaatcaa gttactggac 1500
agtgatcagg agctctaccg caacttcccc ctcaccatct cggagcgggtg gcagcaggag 1560
gtggcagaga ctgtcttcga caccatcaac gctgagacag accggctgga ggctcgcaag 1620
aaagccaaga acaagcagct gggccatgag gaagactacg ccctgggcaa ggactgcatc 1680
atgcatggct acatgtccaa gatgggcaac cccttcctga ccagtgaggc gcggcggtac 1740
ttctacctgt tccccaccg cctcgagtgg cggggcgagg gcgaggcccc gcagagcctg 1800
ctgacctagg aggagatcca gtcgggtggag gagacgcaga tcaaggagcg caagtgcctg 1860
ctcctcaaga tccgcgggtg gaaacagttc attttgcagt gcgatatgca ccctgagctg 1920
gtgcagtgga agaaggagct gcgcgacgcc taccgcgagg ccagcagct ggtgcagcgg 1980

gtgccaaga tgaagaacaa gccgcgctcg cccgtggtgg agctgagcaa ggtgccgctg 2040
gtccagcgcg gcagtgccaa cggcctctga 2070

<210> 48

<211> 689

<212> PRT

<213> Homo sapiens

<220>

<221> ADBR kinase 1

<222> (1)..(689)

<223>

<400> 48

Met Ala Asp Leu Glu Ala Val Leu Ala Asp Val Ser Tyr Leu Met Ala
1 5 10 15

Met Glu Lys Ser Lys Ala Thr Pro Ala Ala Arg Ala Ser Lys Lys Ile
20 25 30

Leu Leu Pro Glu Pro Ser Ile Arg Ser Val Met Gln Lys Tyr Leu Glu
35 40 45

Asp Arg Gly Glu Val Thr Phe Glu Lys Ile Phe Ser Gln Lys Leu Gly
50 55 60

Tyr Leu Leu Phe Arg Asp Phe Cys Leu Asn His Leu Glu Glu Ala Arg
65 70 75 80

Pro Leu Val Glu Phe Tyr Glu Glu Ile Lys Lys Tyr Glu Lys Leu Glu
85 90 95

Thr Glu Glu Glu Arg Val Ala Arg Ser Arg Glu Ile Phe Asp Ser Tyr
100 105 110

Ile Met Lys Glu Leu Leu Ala Cys Ser His Pro Phe Ser Lys Ser Ala
115 120 125

Thr Glu His Val Gln Gly His Leu Gly Lys Lys Gln Val Pro Pro Asp
130 135 140

Leu Phe Gln Pro Tyr Ile Glu Glu Ile Cys Gln Asn Leu Arg Gly Asp
145 150 155 160

Val Phe Gln Lys Phe Ile Glu Ser Asp Lys Phe Thr Arg Phe Cys Gln
165 170 175

Trp Lys Asn Val Glu Leu Asn Ile His Leu Thr Met Asn Asp Phe Ser
180 185 190

Val His Arg Ile Ile Gly Arg Gly Gly Phe Gly Glu Val Tyr Gly Cys
195 200 205

Arg Lys Ala Asp Thr Gly Lys Met Tyr Ala Met Lys Cys Leu Asp Lys
210 215 220

Lys Arg Ile Lys Met Lys Gln Gly Glu Thr Leu Ala Leu Asn Glu Arg
225 230 235 240

Ile Met Leu Ser Leu Val Ser Thr Gly Asp Cys Pro Phe Ile Val Cys
245 250 255

Met Ser Tyr Ala Phe His Thr Pro Asp Lys Leu Ser Phe Ile Leu Asp
260 265 270

Leu Met Asn Gly Gly Asp Leu His Tyr His Leu Ser Gln His Gly Val
275 280 285

Phe Ser Glu Ala Asp Met Arg Phe Tyr Ala Ala Glu Ile Ile Leu Gly
290 295 300

Leu Glu His Met His Asn Arg Phe Val Val Tyr Arg Asp Leu Lys Pro
305 310 315 320

Ala Asn Ile Leu Leu Asp Glu His Gly His Val Arg Ile Ser Asp Leu
325 330 335

Gly Leu Ala Cys Asp Phe Ser Lys Lys Lys Pro His Ala Ser Val Gly
340 345 350

Thr His Gly Tyr Met Ala Pro Glu Val Leu Gln Lys Gly Val Ala Tyr
355 360 365

Asp Ser Ser Ala Asp Trp Phe Ser Leu Gly Cys Met Leu Phe Lys Leu
370 375 380

Leu Arg Gly His Ser Pro Phe Arg Gln His Lys Thr Lys Asp Lys His
 385 390 395 400
 Glu Ile Asp Arg Met Thr Leu Thr Met Ala Val Glu Leu Pro Asp Ser
 405 410 415
 Phe Ser Pro Glu Leu Arg Ser Leu Leu Glu Gly Leu Leu Gln Arg Asp
 420 425 430
 Val Asn Arg Arg Leu Gly Cys Leu Gly Arg Gly Ala Gln Glu Val Lys
 435 440 445
 Glu Ser Pro Phe Phe Arg Ser Leu Asp Trp Gln Met Val Phe Leu Gln
 450 455 460
 Lys Tyr Pro Pro Pro Leu Ile Pro Pro Arg Gly Glu Val Asn Ala Ala
 465 470 475 480
 Asp Ala Phe Asp Ile Gly Ser Phe Asp Glu Glu Asp Thr Lys Gly Ile
 485 490 495
 Lys Leu Leu Asp Ser Asp Gln Glu Leu Tyr Arg Asn Phe Pro Leu Thr
 500 505 510
 Ile Ser Glu Arg Trp Gln Gln Glu Val Ala Glu Thr Val Phe Asp Thr
 515 520 525
 Ile Asn Ala Glu Thr Asp Arg Leu Glu Ala Arg Lys Lys Ala Lys Asn
 530 535 540
 Lys Gln Leu Gly His Glu Glu Asp Tyr Ala Leu Gly Lys Asp Cys Ile
 545 550 555 560
 Met His Gly Tyr Met Ser Lys Met Gly Asn Pro Phe Leu Thr Gln Trp
 565 570 575
 Gln Arg Arg Tyr Phe Tyr Leu Phe Pro Asn Arg Leu Glu Trp Arg Gly
 580 585 590
 Glu Gly Glu Ala Pro Gln Ser Leu Leu Thr Met Glu Glu Ile Gln Ser
 595 600 605
 Val Glu Glu Thr Gln Ile Lys Glu Arg Lys Cys Leu Leu Leu Lys Ile
 610 615 620

Arg Gly Gly Lys Gln Phe Ile Leu Gln Cys Asp Ser Asp Pro Glu Leu
625 630 635 640

Val Gln Trp Lys Lys Glu Leu Arg Asp Ala Tyr Arg Glu Ala Gln Gln
645 650 655

Leu Val Gln Arg Val Pro Lys Met Lys Asn Lys Pro Arg Ser Pro Val
660 665 670

Val Glu Leu Ser Lys Val Pro Leu Val Gln Arg Gly Ser Ala Asn Gly
675 680 685

Leu

<210> 49

<211> 2067

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(2067)

<223> Rat ADBR kinase 2

<400> 49

```
atggcgacc tggaggccgt gctggccgat gtcagttacc tgatggccat ggagaagagc      60
aaggcgaccc cggccgccccg cgccagcaag aggatcgctc tgccggagcc cagtatccgg      120
agtgtgatgc agaagtacct tgcagagaga aatgaaataa cctttgacaa gattttcaat      180
cagaaaattg gtttcttgct atttaaagat ttttgtttga atgaaattaa tgaagctgta      240
cctcaggtga agtttttatga agagataaag gaatatgaaa aacttgataa tgaggaagac      300
cgcctttgca gaagtcgaca aatttatgat gcctacatca tgaaggaact tctttcctgt      360
tcacatcctt tctcaaagca agctgtagaa cacgtacaaa gtcatttatc caagaaacaa      420
gtgacatcaa ctcttttttca gccatacata gaagaaattt gtgaaagcct tcgaggtgac      480
atttttcaaa aatttatgga aagtgacaag ttcactagat tttgtcagtg gaaaaacgtt      540
gaattaaata tccatttgac catgaatgag ttcagtgtgc ataggattat tggacgagga      600
```


<220>

<221> ADBR kinase 2

<222> (1)..(688)

<223>

<400> 50

Met Ala Asp Leu Glu Ala Val Leu Ala Asp Val Ser Tyr Leu Met Ala
1 5 10 15

Met Glu Lys Ser Lys Ala Thr Pro Ala Ala Arg Ala Ser Lys Arg Ile
20 25 30

Val Leu Pro Glu Pro Ser Ile Arg Ser Val Met Gln Lys Tyr Leu Ala
35 40 45

Glu Arg Asn Glu Ile Thr Phe Asp Lys Ile Phe Asn Gln Lys Ile Gly
50 55 60

Phe Leu Leu Phe Lys Asp Phe Cys Leu Asn Glu Ile Asn Glu Ala Val
65 70 75 80

Pro Gln Val Lys Phe Tyr Glu Glu Ile Lys Glu Tyr Glu Lys Leu Asp
85 90 95

Asn Glu Glu Asp Arg Leu Cys Arg Ser Arg Gln Ile Tyr Asp Ala Tyr
100 105 110

Ile Met Lys Glu Leu Leu Ser Cys Ser His Pro Phe Ser Lys Gln Ala
115 120 125

Val Glu His Val Gln Ser His Leu Ser Lys Lys Gln Val Thr Ser Thr
130 135 140

Leu Phe Gln Pro Tyr Ile Glu Glu Ile Cys Glu Ser Leu Arg Gly Asp
145 150 155 160

Ile Phe Gln Lys Phe Met Glu Ser Asp Lys Phe Thr Arg Phe Cys Gln
165 170 175

Trp Lys Asn Val Glu Leu Asn Ile His Leu Thr Met Asn Glu Phe Ser
180 185 190

Val His Arg Ile Ile Gly Arg Gly Gly Phe Gly Glu Val Tyr Gly Cys

195	200	205
Arg Lys Ala Asp Thr Gly Lys Met Tyr Ala Met Lys Cys Leu Asp Lys		
210	215	220
Lys Arg Ile Lys Met Lys Gln Gly Glu Thr Leu Ala Leu Asn Glu Arg		
225	230	235 240
Ile Met Leu Ser Leu Val Ser Thr Gly Asp Cys Pro Phe Ile Val Cys		
	245	250 255
Met Thr Tyr Ala Phe His Thr Pro Asp Lys Leu Cys Phe Ile Leu Asp		
	260	265 270
Leu Met Asn Gly Gly Asp Leu His Tyr His Leu Ser Gln His Gly Val		
	275	280 285
Phe Ser Glu Lys Glu Met Arg Phe Tyr Ala Thr Glu Ile Ile Leu Gly		
	290	295 300
Leu Glu His Met His Asn Arg Phe Val Val Tyr Arg Asp Leu Lys Pro		
305	310	315 320
Ala Asn Ile Leu Leu Asp Glu His Gly His Ala Arg Ile Ser Asp Leu		
	325	330 335
Gly Leu Ala Cys Asp Phe Ser Lys Lys Lys Pro His Ala Ser Val Gly		
	340	345 350
Thr His Gly Tyr Met Ala Pro Glu Val Leu Gln Lys Gly Thr Ala Tyr		
	355	360 365
Asp Ser Ser Ala Asp Trp Phe Ser Leu Gly Cys Met Leu Phe Lys Leu		
	370	375 380
Leu Arg Gly His Ser Pro Phe Arg Gln His Lys Thr Lys Asp Lys His		
385	390	395 400
Glu Ile Asp Arg Met Thr Leu Thr Val Asn Val Glu Leu Pro Asp Thr		
	405	410 415
Phe Ser Pro Glu Leu Lys Ser Leu Leu Glu Gly Leu Leu Gln Arg Asp		
	420	425 430
Val Ser Lys Arg Leu Gly Cys His Gly Gly Gly Ser Gln Glu Val Lys		
	435	440 445

Glu His Ser Phe Phe Lys Gly Val Asp Trp Gln His Val Tyr Leu Gln
450 455 460

Lys Tyr Pro Pro Pro Leu Ile Pro Pro Arg Gly Glu Val Asn Ala Ala
465 470 475 480

Asp Ala Phe Asp Ile Gly Ser Phe Asp Glu Glu Asp Thr Lys Gly Ile
485 490 495

Lys Leu Leu Asp Cys Asp Gln Glu Leu Tyr Lys Asn Phe Pro Leu Val
500 505 510

Ile Ser Glu Arg Trp Gln Gln Glu Val Thr Glu Thr Val Tyr Glu Ala
515 520 525

Val Asn Ala Asp Thr Asp Lys Ile Glu Ala Arg Lys Arg Ala Lys Asn
530 535 540

Lys Gln Leu Gly His Glu Glu Asp Tyr Ala Leu Gly Lys Asp Cys Ile
545 550 555 560

Met His Gly Tyr Met Leu Lys Leu Gly Asn Pro Phe Leu Thr Gln Trp
565 570 575

Gln Arg Arg Tyr Phe Tyr Leu Phe Pro Asn Arg Leu Glu Trp Arg Gly
580 585 590

Glu Gly Glu Ser Arg Gln Asn Leu Leu Thr Met Glu Gln Ile Leu Ser
595 600 605

Val Glu Glu Thr Gln Ile Lys Asp Lys Lys Cys Ile Leu Phe Arg Ile
610 615 620

Lys Gly Gly Lys Gln Phe Val Leu Gln Cys Glu Ser Asp Pro Glu Phe
625 630 635 640

Val Gln Trp Lys Lys Glu Leu Asn Glu Thr Phe Lys Glu Ala Gln Arg
645 650 655

Leu Leu Arg Arg Ala Pro Lys Phe Leu Asn Lys Pro Arg Ser Gly Thr
660 665 670

Val Glu Leu Pro Lys Pro Ser Leu Cys His Arg Asn Ser Ser Gly Leu
675 680 685

<210> 51

<211> 1359

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (1359)

<223> Rat beta Arrestin 1

<400> 51

atgggacgaca aagggacgag ggtgttcaag aaggcgagcc ccaatggaaa gctcaccgtc	60
tatctgggaa agcgggactt tgtggaccac atcgacctcg tggagcccggt ggatggagtgt	120
gttcttgtgg atccggagta tctcaaggag aggagagtct atgtgacgct gacctgcgcc	180
ttccgctacg gccgggagga cctggatgtc ctgggcctga cctttcgcaa ggacctgttt	240
gtggccaacg tgcagtcttt cccgcccggc cctgaggaca agaagcccct gacgcggctg	300
caggagcgcc tcatcaagaa gctgggagag catgcctacc ctttcacctt tgagatccct	360
ccgaacctcc catgctctgt gactttgcag ccgggacctg aagatacagg gaaggcctgc	420
ggtgtggact acgaagtga agccttctgt gcgagaaacc tggaggagaa gatccacaag	480
cggaattctg tgcgcctggt catccggaag gttcagtatg cccagagag gcttggcccc	540
cagcccacgg ccgagaccac caggcagttc ctcatgtcag acaagccctt gcatctggag	600
gcctccctgg acaaggagat ctactaccac ggagaaccca tcagtgtcaa cgtccatgtc	660
accaacaaca ccaacaagac ggtgaagaag atcaagatct cgggtgcgca gtatgcagac	720
atctgtctgt tcaacacagc ccagtacaag tgccctgtgg ccatggaaga ggctgatgac	780
acagtggcac ccagctctac gttctgcaag gtctacacgc tgacccccct cctggccaac	840
aatcgagaga agcggggcct cgccttggac ggggaagctca aacacgagga cacgaacctg	900
gcctccagca ccctgttgag ggaaggagcc aaccgggaga tcctgggcat cattgtttcc	960
tacaaagtga aagtgaagct ggtggtgtct cgtggcggcc tgttgggaga tcttgcaccc	1020
agtgatgtgg ccgtggaact gcctttcacc ctaatgcacc ccaagcccaa agaggaaccc	1080
ccacaccggg aagttccaga gcacgagacg ccggtagata ccaatctcat agaacttgac	1140
accaacgatg acgacattgt gtttgaggac tttgcccgcc agagactaaa aggcatgaag	1200

gatgacaagg aggaagagga ggatggtacc ggctctccgc ggacgcgtga gctcagatct 1260
 cccatgtctc tactggtggt ggtgcttctt tggaattatt ggaaggtaag gaattgccag 1320
 gtggtgcttt cttatccgaa aagaaataaa ttgaattga 1359

<210> 52

<211> 452

<212> PRT

<213> Homo sapiens

<220>

<221> beta Arrestin 1

<222> (1)..(452)

<223>

<400> 52

Met Gly Asp Lys Gly Thr Arg Val Phe Lys Lys Ala Ser Pro Asn Gly
 1 5 10 15

Lys Leu Thr Val Tyr Leu Gly Lys Arg Asp Phe Val Asp His Ile Asp
 20 25 30

Leu Val Glu Pro Val Asp Gly Val Val Leu Val Asp Pro Glu Tyr Leu
 35 40 45

Lys Glu Arg Arg Val Tyr Val Thr Leu Thr Cys Ala Phe Arg Tyr Gly
 50 55 60

Arg Glu Asp Leu Asp Val Leu Gly Leu Thr Phe Arg Lys Asp Leu Phe
 65 70 75 80

Val Ala Asn Val Gln Ser Phe Pro Pro Ala Pro Glu Asp Lys Lys Pro
 85 90 95

Leu Thr Arg Leu Gln Glu Arg Leu Ile Lys Lys Leu Gly Glu His Ala
 100 105 110

Tyr Pro Phe Thr Phe Glu Ile Pro Pro Asn Leu Pro Cys Ser Val Thr
 115 120 125

Leu Gln Pro Gly Pro Glu Asp Thr Gly Lys Ala Cys Gly Val Asp Tyr
130 135 140

Glu Val Lys Ala Phe Cys Ala Glu Asn Leu Glu Glu Lys Ile His Lys
145 150 155 160

Arg Asn Ser Val Arg Leu Val Ile Arg Lys Val Gln Tyr Ala Pro Glu
165 170 175

Arg Pro Gly Pro Gln Pro Thr Ala Glu Thr Thr Arg Gln Phe Leu Met
180 185 190

Ser Asp Lys Pro Leu His Leu Glu Ala Ser Leu Asp Lys Glu Ile Tyr
195 200 205

Tyr His Gly Glu Pro Ile Ser Val Asn Val His Val Thr Asn Asn Thr
210 215 220

Asn Lys Thr Val Lys Lys Ile Lys Ile Ser Val Arg Gln Tyr Ala Asp
225 230 235 240

Ile Cys Leu Phe Asn Thr Ala Gln Tyr Lys Cys Pro Val Ala Met Glu
245 250 255

Glu Ala Asp Asp Thr Val Ala Pro Ser Ser Thr Phe Cys Lys Val Tyr
260 265 270

Thr Leu Thr Pro Phe Leu Ala Asn Asn Arg Glu Lys Arg Gly Leu Ala
275 280 285

Leu Asp Gly Lys Leu Lys His Glu Asp Thr Asn Leu Ala Ser Ser Thr
290 295 300

Leu Leu Arg Glu Gly Ala Asn Arg Glu Ile Leu Gly Ile Ile Val Ser
305 310 315 320

Tyr Lys Val Lys Val Lys Leu Val Val Ser Arg Gly Gly Leu Leu Gly
325 330 335

Asp Leu Ala Ser Ser Asp Val Ala Val Glu Leu Pro Phe Thr Leu Met
340 345 350

His Pro Lys Pro Lys Glu Glu Pro Pro His Arg Glu Val Pro Glu His
355 360 365

Glu Thr Pro Val Asp Thr Asn Leu Ile Glu Leu Asp Thr Asn Asp Asp
370 375 380

Asp Ile Val Phe Glu Asp Phe Ala Arg Gln Arg Leu Lys Gly Met Lys
385 390 395 400

Asp Asp Lys Glu Glu Glu Glu Asp Gly Thr Gly Ser Pro Arg Thr Arg
405 410 415

Glu Leu Arg Ser Pro Met Ser Leu Leu Val Val Val Leu Leu Trp Asn
420 425 430

Tyr Trp Lys Val Arg Asn Cys Gln Val Leu Leu Ser Tyr Pro Lys Arg
435 440 445

Asn Lys Leu Asn
450

<210> 53

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (1233)

<223> Rat beta Arrestin2

<400> 53

atggggtgaaa aaccgaggac cagggtcttc aagaagtcga gccctaactg caagctcacc 60
gtgtacttgg gcaagcgtga ctttgtggat cacttggaca aagtggatcc tgtcgatggg 120
gtggtgcttg tggatcctga ctacttgaag gaccggaaag tgtttgtgac cctcacctgt 180
gccttcgct atggccgaga agacctggat gtactgggcc tgtctttccg caaagatctg 240
ttcatcgcca cctaccaggc ctccccccc atgcccacc cacctcggcc cccacccgc 300
ctacaggacc gactgctgaa gaagttgggc cagcatgcc accccttttt tttcacaata 360
ccccagaatt tgccttgctc cgtcacactg cagccaggac cggaggacac aggggaaggcc 420
tgtggagtag actttgagat tcgagccttc tgtgccaat ctatagaaga aaaaagccac 480

```

aaaaggaact ccgtgoggct tatcatcaga aaggtacagt ttgctcctga gacacccggc    540
ccccagccat cagctgaaac cacacgccac ttctcatgt ctgaccggag gtccctgcac    600
ctagagggtt ccctggacaa agagctgtac taccatgggg aacccctcaa tgtcaacgtc    660
cacgtcacca acaatttctgc caagaccgtc aagaagatca gagtgtctgt gagacagtat    720
gccgacattt gcctcttcag caccgcgcag tacaagtgtc ctgtggctca gcttgaacaa    780
gatgaccagg tgtctcccag ttccacattc tgcaagggtg acaccataac cccgctgctc    840
agtgacaacc gagagaagcg tggccttgcc cttgatgggc aactcaagca cgaagacacc    900
aacctggctt ccagcaccat tgtgaaggag ggagccaaca aggaggtgct gggaatccta    960
gtatcctaca ggggtcaagg gaagctgggt gtgtctcgag gcgggggatgt ctccgtggag   1020
ctacctttcg tcctaattgca cccaagccc cagaccaca tcacccttcc ccgaccccag   1080
tcagcccccc gggaaataga catccctgtg gataccaacc tcattgaatt cgataccaac   1140
tatgccacag acgacgacat cgtgtttgag gactttgcga ggcttcggct gaaggggatg   1200
aaggatgacg actgtgatga ccagttctgc tag                                1233

```

<210> 54

<211> 410

<212> PRT

<213> Homo sapiens

<220>

<221> beta Arrestin2

<222> (1) .. (410)

<223>

<400> 54

```

Met Gly Glu Lys Pro Gly Thr Arg Val Phe Lys Lys Ser Ser Pro Asn
1              5              10              15

```

```

Cys Lys Leu Thr Val Tyr Leu Gly Lys Arg Asp Phe Val Asp His Leu
          20              25              30

```

```

Asp Lys Val Asp Pro Val Asp Gly Val Val Leu Val Asp Pro Asp Tyr
          35              40              45

```

Leu Lys Asp Arg Lys Val Phe Val Thr Leu Thr Cys Ala Phe Arg Tyr
50 55 60

Gly Arg Glu Asp Leu Asp Val Leu Gly Leu Ser Phe Arg Lys Asp Leu
65 70 75 80

Phe Ile Ala Thr Tyr Gln Ala Phe Pro Pro Met Pro Asn Pro Pro Arg
85 90 95

Pro Pro Thr Arg Leu Gln Asp Arg Leu Leu Lys Lys Leu Gly Gln His
100 105 110

Ala His Pro Phe Phe Phe Thr Ile Pro Gln Asn Leu Pro Cys Ser Val
115 120 125

Thr Leu Gln Pro Gly Pro Glu Asp Thr Gly Lys Ala Cys Gly Val Asp
130 135 140

Phe Glu Ile Arg Ala Phe Cys Ala Lys Ser Ile Glu Glu Lys Ser His
145 150 155 160

Lys Arg Asn Ser Val Arg Leu Ile Ile Arg Lys Val Gln Phe Ala Pro
165 170 175

Glu Thr Pro Gly Pro Gln Pro Ser Ala Glu Thr Thr Arg His Phe Leu
180 185 190

Met Ser Asp Arg Arg Ser Leu His Leu Glu Ala Ser Leu Asp Lys Glu
195 200 205

Leu Tyr Tyr His Gly Glu Pro Leu Asn Val Asn Val His Val Thr Asn
210 215 220

Asn Ser Ala Lys Thr Val Lys Lys Ile Arg Val Ser Val Arg Gln Tyr
225 230 235 240

Ala Asp Ile Cys Leu Phe Ser Thr Ala Gln Tyr Lys Cys Pro Val Ala
245 250 255

Gln Leu Glu Gln Asp Asp Gln Val Ser Pro Ser Ser Thr Phe Cys Lys
260 265 270

Val Tyr Thr Ile Thr Pro Leu Leu Ser Asp Asn Arg Glu Lys Arg Gly
275 280 285

Leu Ala Leu Asp Gly Gln Leu Lys His Glu Asp Thr Asn Leu Ala Ser

290 295 300

Ser Thr Ile Val Lys Glu Gly Ala Asn Lys Glu Val Leu Gly Ile Leu
305 310 315 320

Val Ser Tyr Arg Val Lys Val Lys Leu Val Val Ser Arg Gly Gly Asp
325 330 335

Val Ser Val Glu Leu Pro Phe Val Leu Met His Pro Lys Pro His Asp
340 345 350

His Ile Thr Leu Pro Arg Pro Gln Ser Ala Pro Arg Glu Ile Asp Ile
355 360 365

Pro Val Asp Thr Asn Leu Ile Glu Phe Asp Thr Asn Tyr Ala Thr Asp
370 375 380

Asp Asp Ile Val Phe Glu Asp Phe Ala Arg Leu Arg Leu Lys Gly Met
385 390 395 400

Lys Asp Asp Asp Cys Asp Asp Gln Phe Cys
405 410

<210> 55

<211> 2313

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (2313)

<223> human STAT3 : Transcription factor; Phosphorylation by JAK-type k
inases leads to dimersiation and translocation to the nucleus to
transactivate target gene expression

<400> 55

atggcccaat ggaatcagct acagcagctt gacacacggt acctggagca gctccatcag 60

ctctacagtg acagcttccc aatggagctg cggcagtttc tggccccttg gattgagagt 120

caagattggg catatgcggc cagcaaagaa tcacatgcca ctttggtggt tcataatctc 180

ctgggagaga ttgaccagca gtatagccgc ttcctgcaag agtcgaatgt tctctatcag 240

cacaatctac gaagaatcaa gcagtttctt cagagcaggt atctggagaa gccaatggag	300
attgcccgga ttgtggcccg gtgcctgtgg gaagaatcac gccttctaca gactgcagcc	360
actgcggccc agcaaggggg ccaggccaac caccacacag cagccgtggg gacggagaag	420
cagcagatgc tggagcagca ccttcaggat gtccggaaga gagtgcagga tctagaacag	480
aaaatgaaag tggtagagaa tctccaggat gactttgatt tcaactataa aaccctcaag	540
agtcaaggag acatgcaaga tctgaatgga aacaaccagt cagtgaccag gcagaagatg	600
cagcagctgg aacagatgct cactgcgctg gaccagatgc ggagaagcat cgtgagttag	660
ctggcggggc ttttgtcagc gatggagtac gtgcagaaaa ctctcacgga cgaggagctg	720
gctgactgga agaggcggca acagattgcc tgcattggag gcccgcccaa catctgccta	780
gatcggctag aaaactggat aacgtcatta gcagaatctc aacttcagac ccgtcaacaa	840
attaagaaac tggaggagtt gcagcaaaaa gtttcctaca aaggggaccc cattgtacag	900
caccggccga tgctggagga gagaatcgtg gagctgttta gaaacttaat gaaaagtgcc	960
tttgtggtgg agcggcagcc ctgcatgccc atgcatcctg accggcccct cgtcatcaag	1020
accggcgtec agttcactac taaagtcagg ttgctgggtca aattccctga gttgaattat	1080
cagcttaaaa ttaaagtgtg cattgacaaa gactctgggg acgttgcagc tctcagagga	1140
tcccggaaat ttaacattct gggcacaaac acaaaagtga tgaacatgga agaatccaac	1200
aacggcagcc tctctgcaga attcaaacac ttgaccctga gggagcagag atgtgggaat	1260
gggggcccag ccaattgtga tgcttccttg attgtgactg aggagctgca cctgatcacc	1320
tttgagaccg aggtgtatca ccaaggcctc aagattgacc tagagacca ctccttgcca	1380
gttgtggtga tctccaacat ctgtcagatg ccaaatgcct gggcgcccat cctgtggtac	1440
aacatgctga ccaacaatcc caagaatgta aactttttta ccaagccccc aattggaacc	1500
tgggatcaag tggccgaggt cctgagctgg cagttctcct ccaccaccaa gcgaggactg	1560
agcatcgagc agctgactac actggcagag aaactcttgg gacctggtgt gaattattca	1620
gggtgtcaga tcacatgggc taaattttgc aaagaaaaca tggctggcaa gggcttctcc	1680
ttctgggtct ggctggacaa tatcattgac cttgtgaaaa agtacatcct ggcccttttg	1740
aacgaagggt acatcatggg ctttatcagt aaggagcggg agcgggccat cttgagcact	1800
aagcctccag gcaccttctt gctaagattc agtgaaagca gcaaagaagg aggcgtcact	1860
ttcacttggg tggagaagga catcagcggg aagaccaga tccagtcctt ggaaccatac	1920
acaaagcagc agctgaacaa catgtcattt gctaaaatca tcatgggcta taagatcatg	1980
gatgctacca atatcctggg gtctccactg gtctatctct atcctgacat tccaaggag	2040

gaggcattcg gaaagtattg tcggccagag agccaggagc atcctgaagc tgacccaggt 2100
 agcgctgccc catacctgaa gaccaagttt atctgtgtga caccaacgac ctgcagcaat 2160
 accattgacc tgccgatgtc cccccgcact ttagattcat tgatgcagtt tggaaataat 2220
 ggtgaagggtg ctgaaccctc agcaggaggg cagtttgagt ccctcacctt tgacatggag 2280
 ttgacctcgg agtgcgctac ctcccccatg tga 2313

<210> 56

<211> 770

<212> PRT

<213> Homo sapiens

<220>

<221> STAT3 : Transcription factor

<222> (1)..(770)

<223>

<400> 56

Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr Leu Glu
 1 5 10 15

Gln Leu His Gln Leu Tyr Ser Asp Ser Phe Pro Met Glu Leu Arg Gln
 20 25 30

Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala Ala Ser
 35 40 45

Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly Glu Ile
 50 55 60

Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu Tyr Gln
 65 70 75 80

His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr Leu Glu
 85 90 95

Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp Glu Glu
 100 105 110

Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly Gly Gln
115 120 125

Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln Met Leu
130 135 140

Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu Glu Gln
145 150 155 160

Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe Asn Tyr
165 170 175

Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly Asn Asn
180 185 190

Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr
195 200 205

Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala Gly Leu
210 215 220

Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Leu Thr Asp Glu Glu Leu
225 230 235 240

Ala Asp Trp Lys Arg Arg Gln Gln Ile Ala Cys Ile Gly Gly Pro Pro
245 250 255

Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu Ala Glu
260 265 270

Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu Leu Gln
275 280 285

Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met
290 295 300

Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala
305 310 315 320

Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp Arg Pro
325 330 335

Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg Leu Leu
340 345 350

Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val Cys Ile

Asp Lys Asp Ser Gly Asp Val Ala Ala Leu Arg Gly Ser Arg Lys Phe
 370 375 380
 Asn Ile Leu Gly Thr Asn Thr Lys Val Met Asn Met Glu Glu Ser Asn
 385 390 395 400
 Asn Gly Ser Leu Ser Ala Glu Phe Lys His Leu Thr Leu Arg Glu Gln
 405 410 415
 Arg Cys Gly Asn Gly Gly Arg Ala Asn Cys Asp Ala Ser Leu Ile Val
 420 425 430
 Thr Glu Glu Leu His Leu Ile Thr Phe Glu Thr Glu Val Tyr His Gln
 435 440 445
 Gly Leu Lys Ile Asp Leu Glu Thr His Ser Leu Pro Val Val Val Ile
 450 455 460
 Ser Asn Ile Cys Gln Met Pro Asn Ala Trp Ala Ser Ile Leu Trp Tyr
 465 470 475 480
 Asn Met Leu Thr Asn Asn Pro Lys Asn Val Asn Phe Phe Thr Lys Pro
 485 490 495
 Pro Ile Gly Thr Trp Asp Gln Val Ala Glu Val Leu Ser Trp Gln Phe
 500 505 510
 Ser Ser Thr Thr Lys Arg Gly Leu Ser Ile Glu Gln Leu Thr Thr Leu
 515 520 525
 Ala Glu Lys Leu Leu Gly Pro Gly Val Asn Tyr Ser Gly Cys Gln Ile
 530 535 540
 Thr Trp Ala Lys Phe Cys Lys Glu Asn Met Ala Gly Lys Gly Phe Ser
 545 550 555 560
 Phe Trp Val Trp Leu Asp Asn Ile Ile Asp Leu Val Lys Lys Tyr Ile
 565 570 575
 Leu Ala Leu Trp Asn Glu Gly Tyr Ile Met Gly Phe Ile Ser Lys Glu
 580 585 590
 Arg Glu Arg Ala Ile Leu Ser Thr Lys Pro Pro Gly Thr Phe Leu Leu
 595 600 605

Arg Phe Ser Glu Ser Ser Lys Glu Gly Gly Val Thr Phe Thr Trp Val
610 615 620

Glu Lys Asp Ile Ser Gly Lys Thr Gln Ile Gln Ser Val Glu Pro Tyr
625 630 635 640

Thr Lys Gln Gln Leu Asn Asn Met Ser Phe Ala Lys Ile Ile Met Gly
645 650 655

Tyr Lys Ile Met Asp Ala Thr Asn Ile Leu Val Ser Pro Leu Val Tyr
660 665 670

Leu Tyr Pro Asp Ile Pro Lys Glu Glu Ala Phe Gly Lys Tyr Cys Arg
675 680 685

Pro Glu Ser Gln Glu His Pro Glu Ala Asp Pro Gly Ser Ala Ala Pro
690 695 700

Tyr Leu Lys Thr Lys Phe Ile Cys Val Thr Pro Thr Thr Cys Ser Asn
705 710 715 720

Thr Ile Asp Leu Pro Met Ser Pro Arg Thr Leu Asp Ser Leu Met Gln
725 730 735

Phe Gly Asn Asn Gly Glu Gly Ala Glu Pro Ser Ala Gly Gly Gln Phe
740 745 750

Glu Ser Leu Thr Phe Asp Met Glu Leu Thr Ser Glu Cys Ala Thr Ser
755 760 765

Pro Met
770

<210> 57

<211> 774

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (774)

<223> mCIS

<400> 57
atggtcctct gcgtacaggg atcttgctct ttgctggctg tggagcaa at tgggcggcgg 60
cctctgtggg ccagtcctt ggagctgcc gggccagcca tgcagccctt acccactggg 120
gcattcccag aggaagtgac agaggagacc cctgtccagg cagagaatga accgaagggtg 180
ctagaccctg agggggatct gctgtgcata gccaagacgt tctcctacct tcgggaatct 240
gggtggtact ggggttctat tacagccagc gaggcccggc agcacctaca gaagatgccg 300
gagggtacat tcctagttcg agacagcacc caccacagct acctgttcac actgtcagtc 360
aaaaccaccc gtggcccccac caacgtgcgg atcgagtacg ccgattctag cttccggctg 420
gactctaact gcttgtcaag acctcgaatc ctggccttcc cagatgtggg cagccttgtg 480
cagcactatg tggcctcctg tgcagctgac acccggagcg acagcccgga tcctgctccc 540
accccagccc tgcctatgtc taagcaagat gcacctagt actcggtgct gcctatcccc 600
gtggctactg cagtgcacct gaaactgggt cagccctttg tgcgcaggag cagtgcccg 660
agcttacaac atctgtgtcg gctagtcac aaccgtctgg tggccgacgt ggactgctta 720
cccctgcccc ggcgtatggc cgactacctc cgacagtacc ccttccaact ctga 774

<210> 58

<211> 257

<212> PRT

<213> Homo sapiens

<220>

<221> mCIS

<222> (1) .. (257)

<223>

<400> 58

Met Val Leu Cys Val Gln Gly Ser Cys Pro Leu Leu Ala Val Glu Gln
1 5 10 15

Ile Gly Arg Arg Pro Leu Trp Ala Gln Ser Leu Glu Leu Pro Gly Pro

20	25	30
Ala Met Gln Pro Leu Pro Thr Gly Ala Phe Pro Glu Glu Val Thr Glu		
35	40	45
Glu Thr Pro Val Gln Ala Glu Asn Glu Pro Lys Val Leu Asp Pro Glu		
50	55	60
Gly Asp Leu Leu Cys Ile Ala Lys Thr Phe Ser Tyr Leu Arg Glu Ser		
65	70	75
Gly Trp Tyr Trp Gly Ser Ile Thr Ala Ser Glu Ala Arg Gln His Leu		
85	90	95
Gln Lys Met Pro Glu Gly Thr Phe Leu Val Arg Asp Ser Thr His Pro		
100	105	110
Ser Tyr Leu Phe Thr Leu Ser Val Lys Thr Thr Arg Gly Pro Thr Asn		
115	120	125
Val Arg Ile Glu Tyr Ala Asp Ser Ser Phe Arg Leu Asp Ser Asn Cys		
130	135	140
Leu Ser Arg Pro Arg Ile Leu Ala Phe Pro Asp Val Val Ser Leu Val		
145	150	155
Gln His Tyr Val Ala Ser Cys Ala Ala Asp Thr Arg Ser Asp Ser Pro		
165	170	175
Asp Pro Ala Pro Thr Pro Ala Leu Pro Met Ser Lys Gln Asp Ala Pro		
180	185	190
Ser Asp Ser Val Leu Pro Ile Pro Val Ala Thr Ala Val His Leu Lys		
195	200	205
Leu Val Gln Pro Phe Val Arg Arg Ser Ser Ala Arg Ser Leu Gln His		
210	215	220
Leu Cys Arg Leu Val Ile Asn Arg Leu Val Ala Asp Val Asp Cys Leu		
225	230	235
Pro Leu Pro Arg Arg Met Ala Asp Tyr Leu Arg Gln Tyr Pro Phe Gln		
245	250	255
Leu		

<210> 59
 <211> 639
 <212> DNA
 <213> Homo sapiens

<220>
 <221> gene
 <222> (1) .. (639)
 <223> mSOCS1

<400> 59
 atggtagcac gcaaccaggt ggcagccgac aatgcgatct ccccggcagc agagccccga 60
 cggcgggtcag agccctcctc gtccctcgtct tcgtccctcgc cagcggcccc cgtgcgtccc 120
 cggccctgcc cggcgggtccc agccccagcc cctggcgaca ctcaacttccg caccttccgc 180
 tcccactccg attaccggcg catcacgcgg accagcgcgc tcctggacgc ctgcggcttc 240
 tattggggac ccttgagcgt gcacggggcg cacgagcggc tgcgtgccga gcccggtgggc 300
 accttcttgg tgcgcgacag tcgccaacgg aactgcttct tcgcgctcag cgtgaagatg 360
 gcttcggggc ccacgagcat ccgcgtgcac ttccaggccg gccgcttcca cttggacggc 420
 agccgcgaga ccttcgactg ccttttctgag ctgctggagc actacgtggc ggcgccgcgc 480
 cgcattgttg gggccccgct gcgccagcgc cgcgtgcggc cgctgcagga gctgtgtcgc 540
 cagcgcacgc tggccgccgt gggtcgcgag aacctggcgc gcatccctct taaccggta 600
 ctccgtgact acctgagttc cttccccttc cagatctga 639

<210> 60
 <211> 212
 <212> PRT
 <213> Homo sapiens

<220>
 <221> mSOCS1

<222> (1) .. (212)

<223>

<400> 60

Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala
1 5 10 15

Ala Glu Pro Arg Arg Arg Ser Glu Pro Ser Ser Ser Ser Ser Ser Ser
20 25 30

Ser Pro Ala Ala Pro Val Arg Pro Arg Pro Cys Pro Ala Val Pro Ala
35 40 45

Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp
50 55 60

Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe
65 70 75 80

Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala
85 90 95

Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys
100 105 110

Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg
115 120 125

Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr
130 135 140

Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg
145 150 155 160

Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln
165 170 175

Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu
180 185 190

Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe
195 200 205

Pro Phe Gln Ile

210

<210> 61

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> linker sequence

<400> 61
gggccacgaa

10

<210> 62

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> linker sequence

<400> 62
ttcgtggccc ctg

13

<210> 63

<211> 138

<212> DNA

<213> Artificial Sequence

<220>

<223> pP6 vector sequence

<400> 63
ctagccatgg ccgcaggggc cgcggccgca ctagtgggga tccttaatta aaggggccact 60
ggggcccccg gtaccggcgt ccccggcgcc ggcgtgatca cccctaggaa ttaatttccc 120
ggtgaccccg ggggagct 138

<210> 64

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> pB6 vector sequence (5'-3')

<400> 64
catggccgga cgggccgcgg ccgcactagt ggggacccctt aattaaaggg ccactggggc 60
cccc 64

<210> 65

<211> 76

<212> DNA

<213> Artificial sequence

<220>

<223> pB20 vector sequence (5'-3')

<400> 65
aattcggggc cggacgggcc gcggccgcac tagtggggat ccttaattaa gggccactgg 60
ggcccctcga cctgca 76

<210> 66

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 66
gcgttttgaa tcactacagg 20

<210> 67

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 67

cacgatgcac gttgaagtg

19